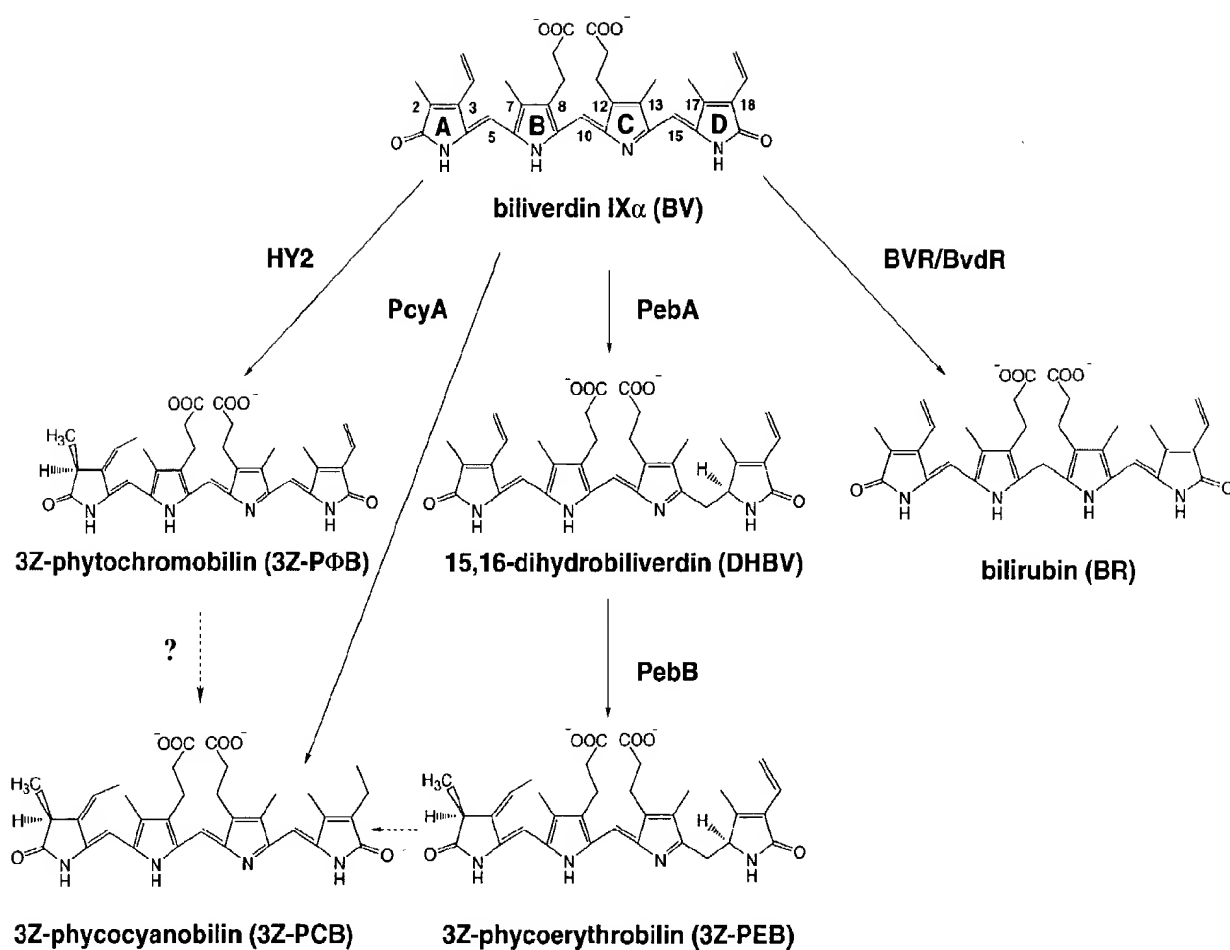
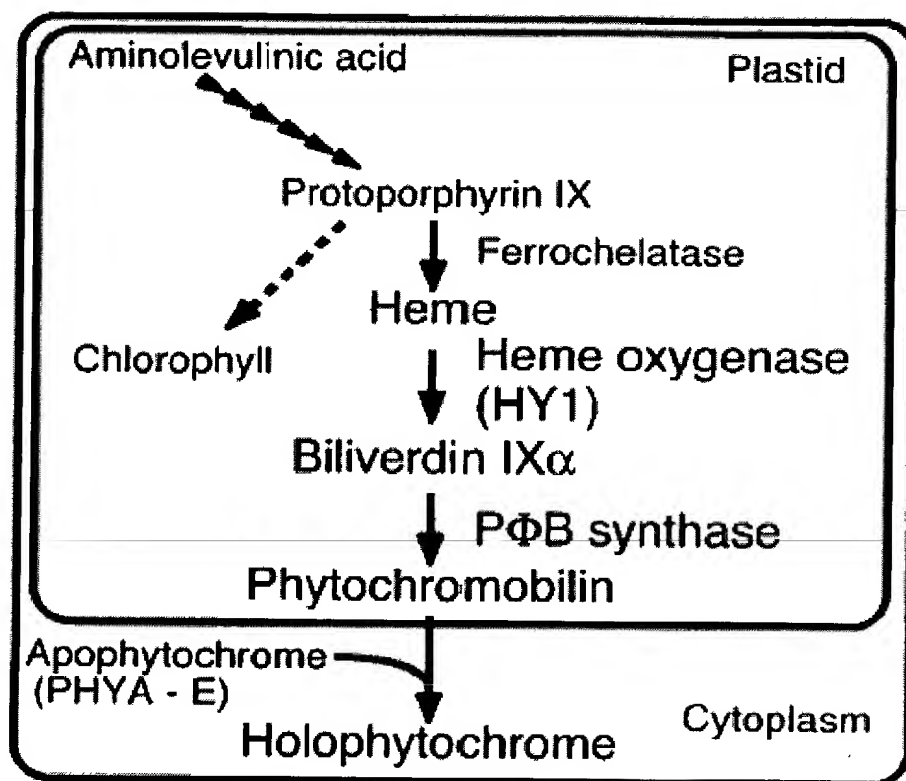


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**Fig. 1**

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**Fig. 2**



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gaattccccacgtcaacgtgactgtgcattccacgtggcggatgtgggacctatagttgg 60  
accatgactoggacggatgttgaaattcattgtcgttgccaattgcgtttgtctcactga 120  
aactgtgaaaattttatctcttttatagataaAGAATCTTGCTTTTTTCAGTTTTTCAGTA 180  
TGAAGAAGAATTGAAGAGAGTGTCCGAGGAAGGAGACCTTTGGTTTCAGTTTGTGAGTCT 240  
TGTTGTAATGGCTTTATCAATGGAGTTTGGGTTTTC AATTGGGTCATGCTTCAAGGCACC 300  
M A L S M E F G F S I G S C F K A P  
AAACCCACCTGTTCTAATCTCTGCAAGCCCTAATAAGATCAATTTACGTTGAGAAGGAG 360  
N P P V L I S A S P N K I N F T L R R R  
AAAGAAAAGATTCTTACTTAGAGTCTCTGCTGTGTCTGATAAGGAATTCGCAGAGTCTGC 420  
hy2-106 \*\*\*\*\*  
K K R F L L R V S A V S Y K E F A E S A  
TTTAGAAGAAACCAGGAAAAGGATCGTTCTTGAACCTTCACATCTCCAGgtatatgcaat 480  
L E E T R K R I V L E P S H L Q  
tacatttcgttagtgtagtgggaggattatatatttctcattgtttcttgctgtgaatttg 540  
ggtaaattgatttgagttgtcattaggaaccaaaacaataactttactgttatagactgc 600  
ttatataagtaaaagttcagattttgtttttctaatcacgaaactgttttcagGAAAAGTA 660  
E K Y  
TAGTAGCATGACAGGACTAGATGGTAAGACCGAACTTCAAATGCTTGCTTTTAAATCTTC 720  
S S M T G L D G K T E L Q M L A F K S S  
AAAGATTAGACTCTTGAGGAGTATGGCAATAGAGAATGAGACAATGCAGgtttaacttca 780  
K I R L L R S M A I E N E T M Q  
gcagtacaaactgattgcttttagtcccatttcccttactttcaattgattgattgtttgta 840  
hy2-105 \*\*\*\*\*  
tcttcgcttagGTCTTTGACTTTGCGGGTTTCATGGAGCCTGAGTATGATACTCCCATAT 900  
hy2-1,hy2-104 T  
V F D F A G F M E P E Y D T P I F  
TCTGTGCTAACTTTTTTCACATCTACCAACGTTAACATAGTTGTATTgtaagttatcttct 960  
C A N F F T S T N V N I V V L  
agttatgctggagttatcaggtctgtattgtccaaactgatgttcaatattttactgtat 1020

Fig. 3B



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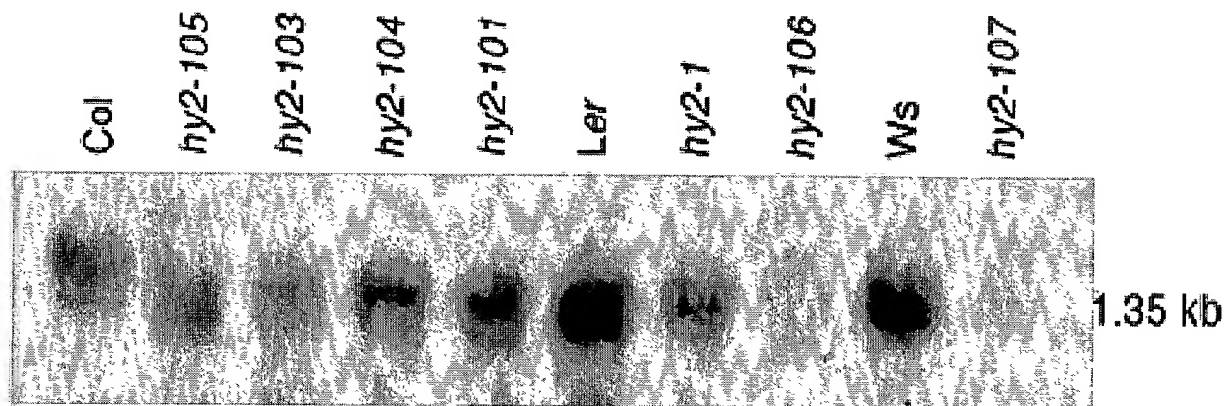
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D L N P L H Q L T D Q T D Y Q D  
CAAGTATTATAACAAGATAATGTCCATATATCACAAATATGCTGAGgtgaccacaangaat 1140  
K Y Y N K I M S I Y H K Y A E  
acaccaaattactcaattgcaagtaaaccotaatgctgaggtgtaaatgactgatcttgag 1200  
atttatttgcagACTTTCCCATGGGGAGGGAAATTGACTGGTGAATCCATAAAGTTTTC 1260  
hy2-101 A  
T F P W G G K L T G E S I K F F  
TCGCCTTTGGTGATGTGGACTAGGTTTTCGTCTAGCAAAGAAAAACATAAGGCTTTGTTTC 1320  
S P L V M W T R F S S S K E K H K A L F  
TCTGCGTTTCTAGAGTACTATCAGgtatatactcagcgggccaaaagctaagggtttttattg 1380  
S A F L E Y Y Q  
gaaactttgactgagaatctatcatcttcttcttctacagGCATGGCTTGAGATGACAATCC 1440  
hy2-107 a  
A W L E M T I Q  
AAGTGAGGGAGGAGATGGAACCATCTCATGTGAGAGCCAATTGTGAAGCACAAACACAAGT 1500  
V R E E M E P S H V R A N C E A Q H K Y  
ACCTGACATGGCGAGCACAAAAGgtgatttcatttccttttgtgtaatttgcatgtttga 1560  
hy2-103 A  
L T W R A Q K  
acagacactgtatctgtattgttacaantggatattgatttggtggttgagGATCCTGGA 1620  
hy2-102 a  
D P G  
CATGGTCTTCTTAAAAGATTAGTAGGTGAAGCAAAGGCCAAAGgtataaaagatttgatcc 1680  
H G L L K R L V G E A K A K  
cattagtgccccattattaattagcttgtgaagatggttgaaaatgatttgaacaaatc 1740  
agGAGCTGCTAAGGGATTTCCTGTTCAATGGGGTGGATGAGTTAGGCACAAAAACATTCA 1800  
E L L R D F L F N G V D E L G T K T F I  
TTGATTACTTTCCAGAGTACCAAACAGAAGATGGAAGTGTAAAGCGATAAACGAAGTATCA 1860  
D Y F P E Y Q T E D G T V S D K R S I I  
TTGGGAAGTCATATGAAACTCGTCCATGGGATTTAACAGGACAATTTATCGGCTAACAAAT 1920  
G K S Y E T R P W D L T G Q F I G ==  
GATATATGTGAACAAGTCAGATTTTCAGAGTCATCAACACAAGAGGACGTGAACCTTAGGGA 1980  
AGTAGGAATAAGAAAGAGCAGCATGAGGAGTCTCTCAGGTCTATCTGCATTTCAAGATGA 2040  
TTGTTTGAGTTACCATGCATTGTAGTTTTACAAGTGTAGCTCTCAGCCCTTCATCAAAAT 2100  
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**Fig. 3B cont'd.**

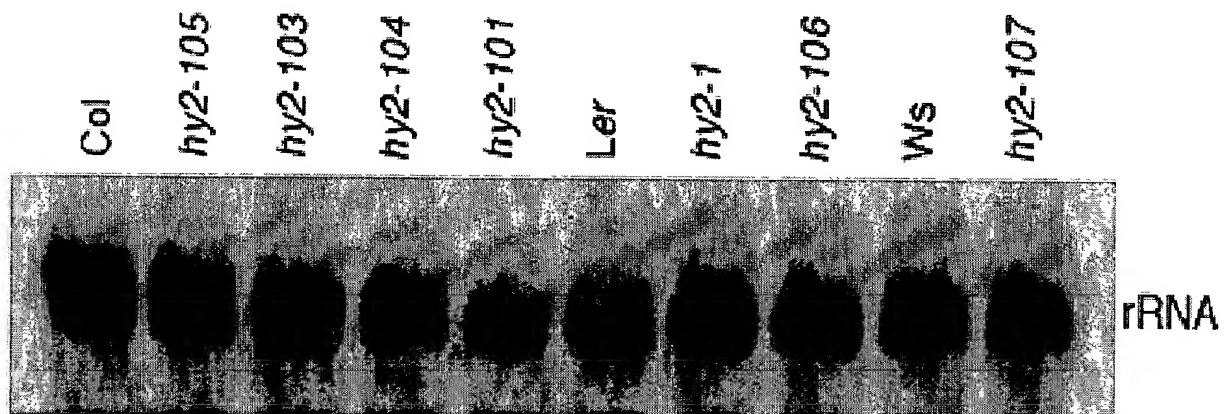


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**Fig. 4A**



**Fig. 4B**



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```

*                20                *                40
HY2_ARATH : MALSMEFGFSIGSCFKAPNPPVLI SASPNKINFTLRRRKK
YCP2_SYNPY : -----
YHP2_PROMA : -----
YHP3_PROMA : -----MI I KR DNS
YCP3_SYNPY : -----MTNQRFKS
SLR0116 : -----MAVTDLSLTN

```

```

*                60                *                80
RFLLR SAVSYKEFAESALEETRKRI VLEESHLEQEKYSSMTGLDGK - : 86
-----FDSFLNELHSDITKR-----GGSFLPLPEGLEECRSSKSS - : 36
-----LNKLMLQDLHNNLKRRRI-ISHGCKPIEVENGMSERFSSHKQD - : 40
LSKID ERDWIWT PFFNDLV DKL-SVFEIE PYPVSHDFLSKESITGSR : 54
TDPVN EGSWSWQPFLEDAIKRL-EGLNVE PYPVPDRFLQREDQTGSK : 54
SSLMP TLNPMIQQLALALIAASW-QSLPLKPYQLPEDLGYVEGRLEGE : 56
P 6

```

```

*                100                *                120
HY2_ARATH : -----TELQMLAEKSSKRIQLLRSMADEN-ETMQVDFDFAGE
YCP2_SYNPY : -----SVIQSWLWDVPGERRWRVTRDAGDSQOVENS VAY
YHP2_PROMA : -----TVIKSWLWDVPGERRWRVTRDAGDKQVLS VAY
YHP3_PROMA : RNPVHVTTLTWAAKFEKIKQVRLAC KGGESLSVFNLIH
YCP3_SYNPY : SKSIPVTTATWACKTEKFRQVLAACVSAAGSAASVLFVIN
SLR0116 : -K-----LVLENRCYQTPQFRKMHL ELAKVKGDDILHCVMF
P 4 r g 6

```

```

*                140                *                160                *
MEPEYDTPIFCANFFSTSTNVN--VVMIDLNELHQLTDQTDYQDKYMN : 165
PDYNDRPLMGVDLWFGARQKLAVVDFQPLVQ---DKDYLDRYYS : 115
PAYTNDKPILCIDIFWFG LKRKLAVVDFQPLVQ---EERYFCRYVK : 119
PLNDV DLPFFGADFWTL PNG--HLLADLQPAKL--DNIHTENVVP : 137
PKSTYGLFFFGGLVTFPAG--HLLADLQPAIKT--DEVHTTHVAD : 137
PEPLMGLFLFGCDIVAGPGG-VSAATADLSBTQS---DRQLPAAYQK : 135
P Y P g l 1 D P

```

Fig. 5



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```
180          *          200          *
HY2_ARATH   : KIM----SYHKVAETTPWGCKLTGESIKNSPLVMTR-
YCP2_SYNPY  : GLK----EYNQRIPDLNGEETMRSTDPNQYESWLLCR-
YHP2_PROMA  : DLQ----ILKNRIVDFNSQKTMKIYDSNKIESPWVLLYN-
YHP3_PROMA  : RLI----PLHDHMQSLLPSGGEIPKEAEFYESPGFLSRL
YCP3_SYNPY  : RLI----PLFERWRDQLPYGGPIPEEAQFEESPGFLWTRL
SLR0116     : SLAELGQPEFEQQRELPPWG-----EIESEYCLAIR-
              6                      FS          6  X
```

```
220          *          240          *          260
---FSSSKEKHKAIFSAFLENYQANLEMTIQVREEMEPSHVRANCA : 244
---GGAEQADLSIPKATSAIKAYWDIHDNAKSIPSTIPPEEVKNL : 193
---GSFDDLQCSIAKILDEIHAHWQDNNNSREYIKIIPSKVEGL : 197
PLSKESDNIISEIRPAFGEYISLYIEILHIAPLKKEK-ALKILEG : 219
PLGEEGDELIQSIVRPAFENDYLDLLELAASAERVTDER-SEVLLG : 219
----PSNVTEERFVQRVVDLQIHCQSIVAEPLSEAO-TLEHRG : 208
              51
```

```
          *          280          *          300
HY2_ARATH   : QHKYLTARAQKDPGHGLKKRLVGEAKAKELLRDFLENGVD
YCP2_SYNPY  : QDKYDIYSAERDPAHGLFTSHFGKDWNSNRELHEFLPASP
YHP2_PROMA  : HINIDIYSAERDPAHGLFKSYFCQTADQVREFLEPHSH
YHP3_PROMA  : QKAYINRSTKDFARAMLCRFYCKEWTEDYIHKVLENI--
YCP3_SYNPY  : QRKYTDYRAEKDPAARGMLTREHCSSETEAMIHTVLEDDL--
SLR0116     : QIHYCQQQOKNDKTRRYLEKAFGEAARAERMMSQVLEDDVIQ
              Q  Y          Dp  6          G  W          6  LF
```

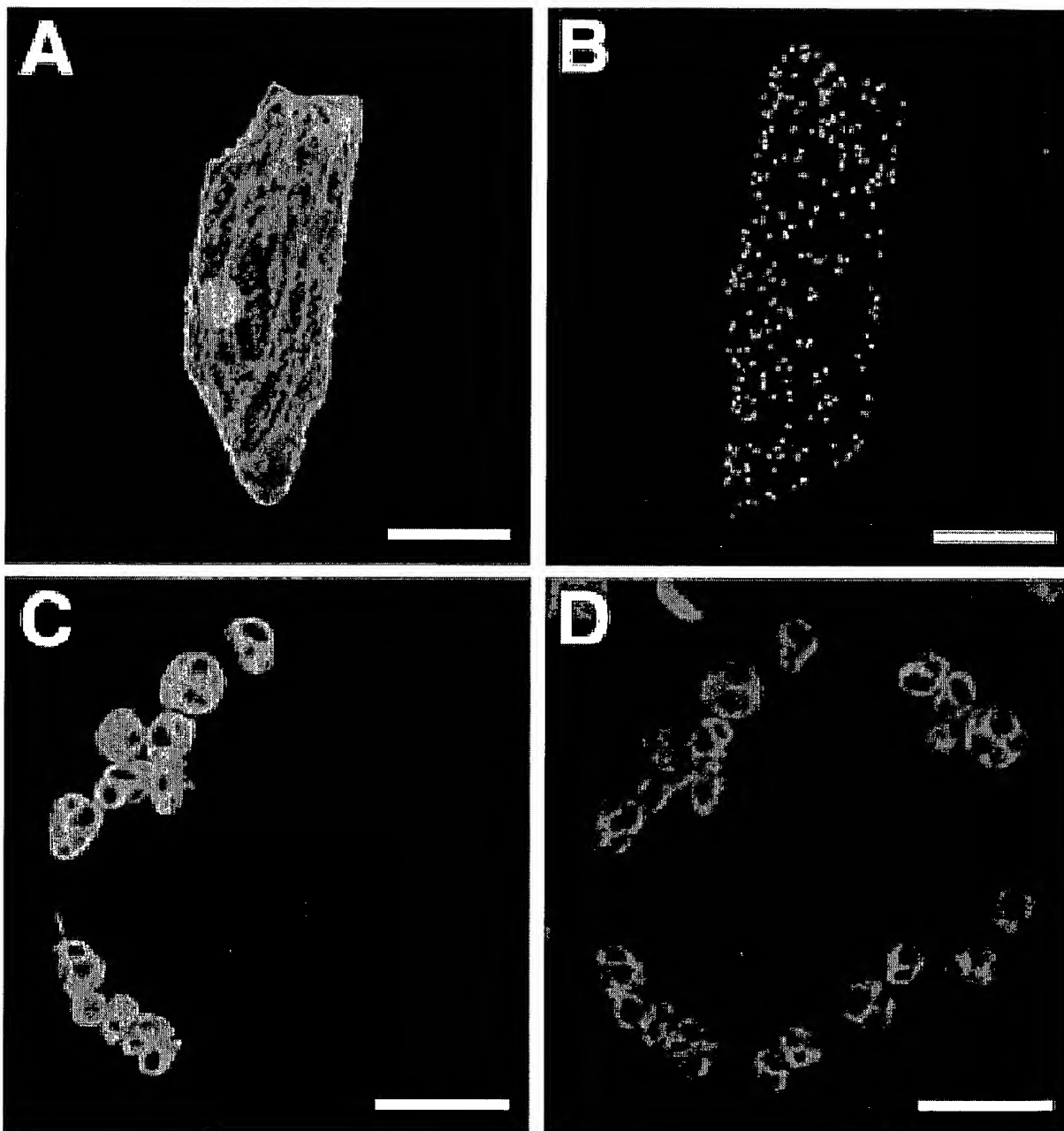
```
          *          320          *          340
ELGTKTFIDYFPEYQTEDGTVSDKRSIIGKSYETRPWDLTGQFIG : 329
SHK----- : 236
LTAD----- : 241
----- : 257
----- : 257
----- : 248
```

Fig. 5 cont'd.



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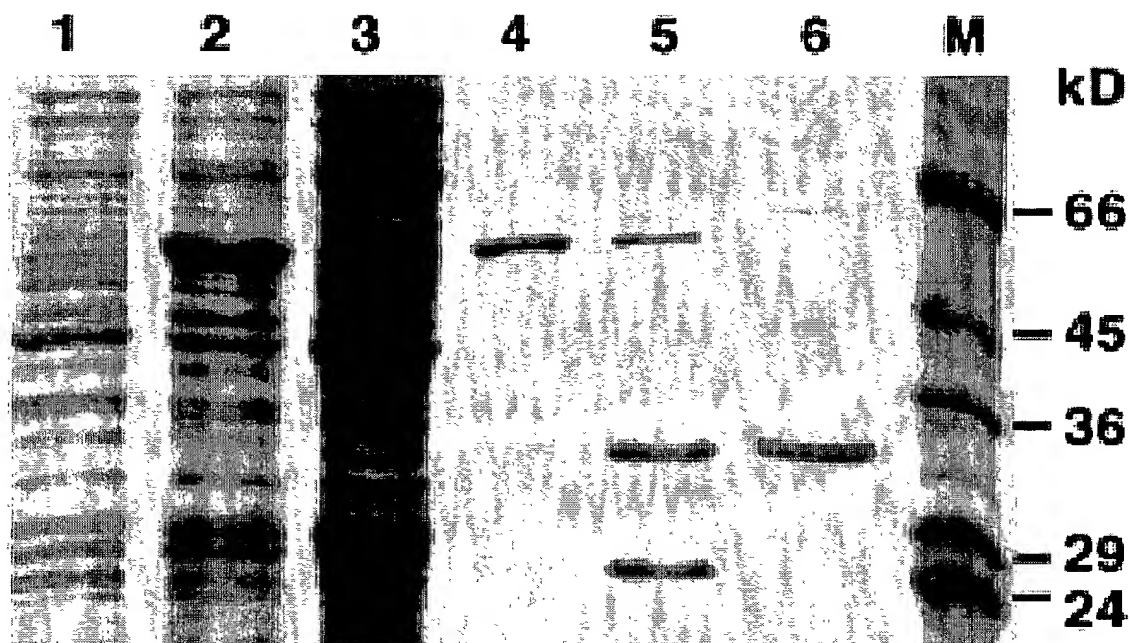


**Fig. 6**





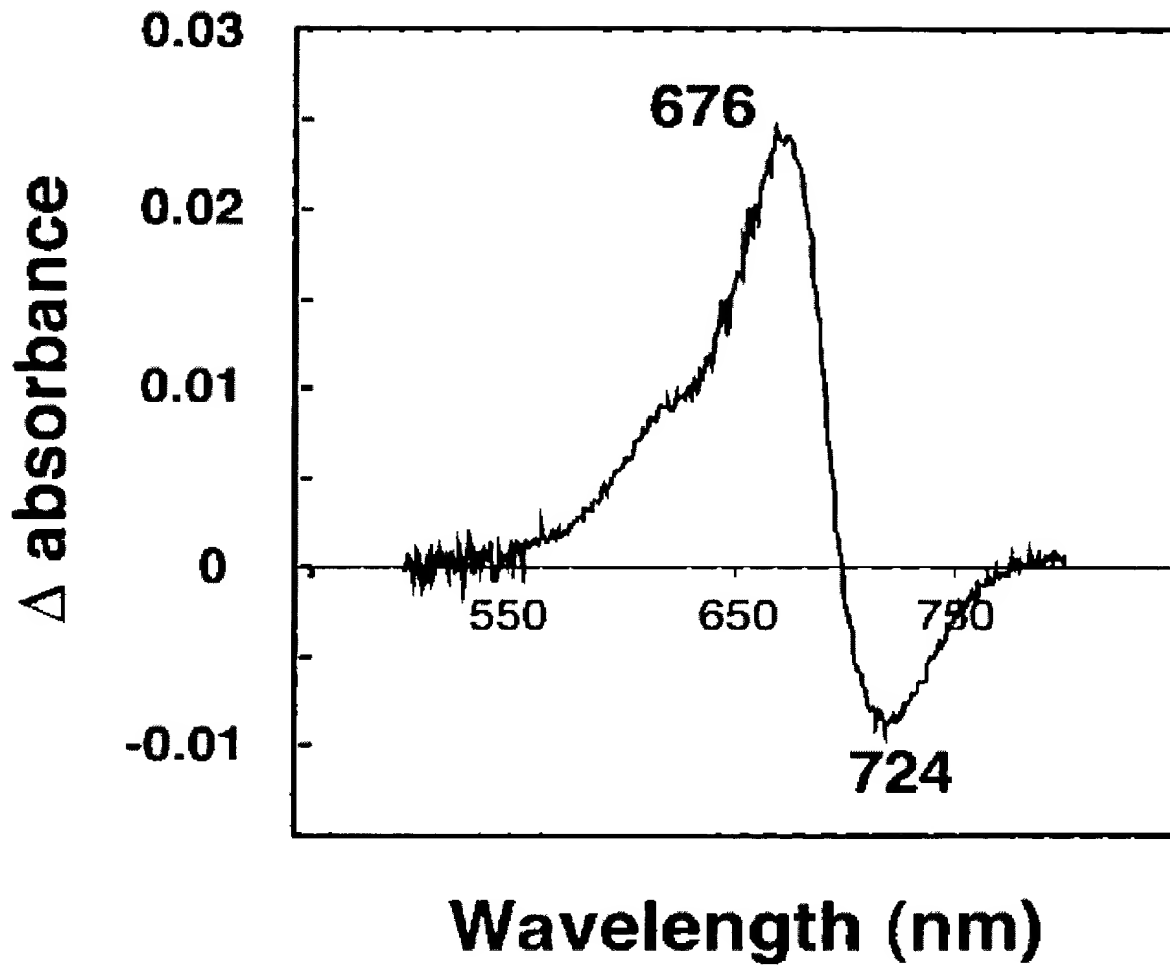
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**Fig. 7**



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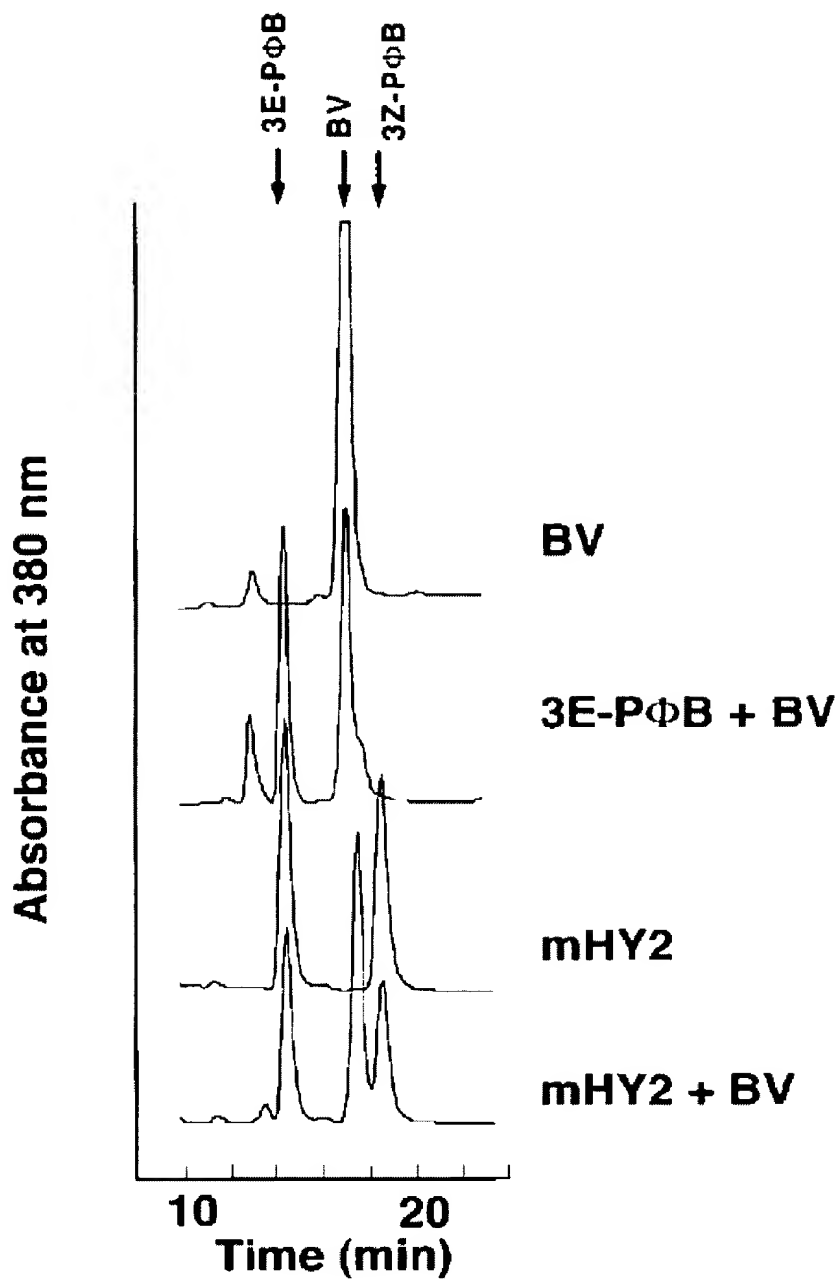


**Fig. 8**

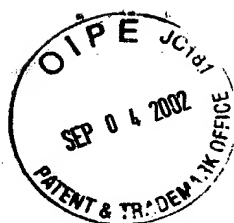


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**Fig. 9**



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```

*                20                *                40
Pcya_ANASP : -----
Pcya_NOSPU : -----
Pcya_SYNY3 : -----
Pcya_SYNB1 : -----
Pcya_PROMA : -----
Peba_SYNPY : -----
Peba_SYNB1 : -----
Peba_PROMA : -----
Peba_PROMA : -----
Peba_NOSPU : -----
PebB_SYNPY : -----
PebB_SYNB1 : -----
PebB_PROMA : -----
PebB_PROMA : -----
PebB_NOSPU : -----
HY2_ARATH : -----MALSMEEFGESIGSCFKAPN-PPVLISA
RCCR_ARATH : MAMIFCNTLYSSSSPSYLSPLTSKPSRFSKNLRPRAQFQS
RCCR_HORVU : -----

```

```

*                60                *                80                *
-----MSLTSIPSLREQQHPHIRQLADCHIEVWHQHLDLSPYHHPAEL : 43
-----MSFTSMPSLREQQHPHIRQLADCHIEAANHQHLDLSPYHHPDEL : 43
---MAVTDLSLTNSSLMPITLNPMTIQQLALATAASNQS-LPLKPYQLPEDL : 46
-----MQSPPESSSSTVAPHTIPSLAETIRGAWIGLPELKPLDADSDF : 42
-----LNLLSRSLTKTKLIDPHTILTLLQNTKVKVRSKLNDELNCIEVDPKL : 44
-----MFDSPLNEEHSDITK-RGGSPLEFLPEGL : 27
-----MFDPFLEELGTGTOA-RGGISVEVPAGL : 27
-----MNKLLQLDLHNNFKRRTIS-HGGKRIEVENGM : 31
-----MFESLKNFMKTNIE---DLDGKELEISK : 25
INETCMIAITYFHARVKNKSCSYKPFLEFLKELFQRFDLQSRVPIPEGL : 64
----MTNQRFKSTDPVNIEGWSWQPFLEDAIKRLEG-LNVERYPVPDFR : 44
---MSIDLRASSLDPVQIPGWRWQPFLEASAAKLP-FNPSYPPIAETF : 45
----MIIKRDNLSKIDLRDWTPTPFNDIVDKLSV-FETEPYPVSHDF : 44
-----MLIQNTIFYSQEWRWAKFIKFIISQLDN-YHCVENKIASDF : 40
-----MNSERSDVTIYQPFLDYAIAYMRSRLDLEPYPIPTGF : 37
KINFTLRRRKERFLLRVSAVSKEFAESAEETRKR-IVLEPSHLQEKY : 77
HDDHLRRKFMEFPYVSPTRKQIMVDLMSTVENRLQS--QLLPCNLPPDV : 90
-----

```

Fig. 10



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```
100 * 120 *
PcyA_ANASP : GYVEGRLEGEK- - - - - LTIENRCYQTPQF KKHLELAKV
PcyA_NOSPU : GYVEGRLEGEK- - - - - LTIENRCYQTPQF KKHLELANI
PcyA_SYNY3 : GYVEGRLEGEK- - - - - LVIENRCYQTPQF KKHLELAKV
PcyA_SYN81 : SSI EGQLEGGD- - - - - LLIRNELLCRCGV KKHLELARL
PcyA_PROME : SNI ISNEEGKE- - - - - LYIENEFYKAKCF KKLHIEVAEPS
Peba_SYNPY : EECRSSKSS- - - - - SVIQSWLWDVPCF ERWRVTRLDA
Peba_SYN81 : EHNQSQKGS- - - - - STIQSWLWDVPCF ERWRVTRLDA
Peba_PROMA : SERFSHKQD- - - - - TVIKSWLWDVPCF ERWRVTRMDA
Peba_PROME : EFKEHHNKD- - - - - SKYIILKNWIFESQQY KKWRTKLDG
Peba_NOSPU : EFKVSDRGR- - - - - NPATIRSWCYQSOEL KXIRYTYIDA
Pebb_SYNPY : LQREDQTGSKSK-SIPVTTATWACKTEKF QVRAACVSA
Pebb_SYN81 : LQKEGSTGSKAK-PVPVTTATWACSTDKL QVRCACVEA
Pebb_PROMA : LSKESITGSRN-PVHVTTLTWAAKF EKI QVRLAC LKGC
Pebb_PROME : SYKESSYGSKKS-KKNINLFTWGATHQKRINFARAVCINS
Pebb_NOSPU : ESN SAVVGKGN-QEEVVTTSYAFQTALR QIRAAHVQC
HY2_ARATH : SSMTGLDG- - - - - KTELQMLAEKSSKIELLRSMATEN-
RCCR_ARATH : RNFNNPNGSAAEASLHIRSGDKSSPIDFVIGSWIHCKIPTC
RCCR_HORVU : - - - - - MDEFNLQSSSLHCKVPE
```

9

```
140 * 160 * 180
NMEDILHCVMEPRPEYDLPMFEC DIVGGR-GQISAAADLS PVHL- - - - - BRTL : 126
NMEDILHCVMEPRPQNNLPMFEC DIVGGR-GQISAAADLS PIQL- - - - - BRTL : 126
KGLDILHCVMEPEPLYGDLPMFEC DIVAGP-GGVSAADLS PTQS- - - - - DRQL : 129
RGLOILHCVMEPRPDLPMFEC DIVAGP-AGVSAADLS PV- - - - - SGTL : 123
KSKILHCVMEPRDPKMDIPIEGM DIVKVN-ELVSAADLS SSK- - - - - NQNL : 127
DSLQVNSVAMEPDYNMPLMGLV DILLWFGARQKLAVLD FQPLVQ- - - - - DKDY : 109
DSLQVNSVAMEPFDLDNPLMGLV DILLWFGARQKLAVLD FQPLVQ- - - - - DKDY : 109
DKLQVNSVAMPAYTNDKPILEI DILLWFGGLKRKLAVLD FQPLVQ- - - - - EERY : 113
DKLQVNTVARENFKSESPILEI DILLWFGTSQKLAVLD FQPLVQ- - - - - EKKY : 109
ESAQIFNSVWYPSHNYDLPLGLI DFLSFG-KVKNLAVLD FQPLVQ- - - - - DEDY : 147
SAASVLENFVINEKSTYGLPFEGG DIVTFP-AGHLLALDLQPAIK- - - - - TDEVH : 131
MAASVLENFVINPSCREDEPFEGG DIVTLP-NGHLLALDLQPVOK- - - - - ADPDH : 132
ESSEVFNLLIHPLNDYDLPFEGG DIVTLP-NGHLLALDLQPAIK- - - - - LDNIH : 131
FNYSVLENFVILIPKTSYNIPLGLV DIVSLP-TSHLLVLD FQPSLK- - - - - VENQF : 127
NSLQVLENFVIEPHLNYDLPFEGG DIVTLP-GGHLLALDLQPLFR- - - - - DESAY : 124
ETMQVDFEAGREMEPEYDTPIECANFTST- - - - - MVNVLVLDLNPPLHQLTDQTDY : 159
VSLNITISISGLNSSTKAPNEVVEIQSS-SKSLVLDLPHRKDLVLNPDY : 181
-ADLITSLFINLNASTDAPEIMEFIQGS-PTSMVLDLPHRKDLALHPEY : 66
```

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Fig. 10 cont'd.



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```
                200                *                220
PcyA_ANASP : PESYNSAITSNT---LNFSQPRELPWGNI----FSDF
PcyA_NOSPU : PESYTTALAQLPV---LNFSQPRELPWGNI----FSDF
PcyA_SYNY3 : PAAYOKSLAELGQ---PEFEQQRELPPWGEI----FSBY
PcyA_SYNB1 : PSGLETAAGTPS---PAFRQVRDLPGWGTI----FSBH
PcyA_PROME : --KYDHL LSH LDK---SVFKSKREIPIWGNI----FSKN
PebA_SYNPFY : LDRYFSG LKE LNQRF PDLNGEETMRSFDPNQY----ESSW
PebA_SYNB1 : LDRHFDGLKDLNARF PDLNGEETMRSFDPNQY----ESSW
PebA_PROMA : FCRYYKDLQIEKNRFVDFNSQKTKIYVSNKY----FSPW
PebA_PROME : LQKYCSS LDF LKNOY SVFDNHKMKNIYVSKKY----FSPW
PebA_NOSPU : QNKYIAP LKY LHNKY PDLAQNLEMKFYMANQY----FSKY
PebB_SYNPFY : TTHVWDR LIP LFERWRDQLPYGGPIPEBAQPF----FSPG
PebB_SYNB1 : TQFVWER LMP LFERWQAE LFDGGPIPEBAQPF----FSPA
PebB_PROMA : TENVWPR LIP LPHDHWQSL LPSGGEI PKBAEPY----FSPG
PebB_PROME : NSELLEQ LK LKKSCHSSL PVAEKMS EFWAKY----FSPG
PebB_NOSPU : QAKYTEP LIP LFAHQHL SWGGDFPEBAQPF----FSPA
HY2_ARATH : QDKYYNK LMS LHKYAETF PWGGKLTGSSIKY----ESPL
RCCR_ARATH : LKEYYQDTALDSHRQS LK LK LPEVNDYVSPSLFVRSAESPT
RCCR_HORVU : IEKYYEDTEVDKQRKIIEQLPQARPYLSPSLFVRSAESPT
                4                FS
```

```
                *                240                *                260                *
CQVVRP-----SSPEEEAMFIGRVREPLQVHCQGAIAA--SPVSAEQK : 199
CQVVRP-----GSPEEEAMFLSRVREPLDIHMQAIAA--HPVSVEQV : 199
CQVVRP-----SNVTEERFVQRVVDLQIHCHQSIVA--EPLESAQT : 202
VQVVRP-----DGAEELVLFPSRVREPLDILRTAVLQTACEPATAAST : 198
MFAASL-----KNESEKNAFCKIVDNVLSVLIQLSQST--SPDSDEYI : 198
ILDFCRG-----CAEQADLS LPKAFSAFLKAYNDLHDNA--KSIPSTIP : 186
ILDFCRG-----GSSEADRS LPKAFSAFLKAYNGLHDEA--SKEPSSIS : 186
WLYRNG-----SFDDLQCS LAKILDEPLHAYWQVDNNN--SREYIKIT : 190
VMICRG-----NKLNLDRDLNNIFCSFVSNNLTINKIH--ONNOFLD : 185
LDFAKT-----DAETVSTRVFEAFQDYLNLYWQMLADA--QALHDPED : 224
FLWTR LPLGE---EGDELIQSI VEPAFNEYIDELYLELAASA--ERVTDERS : 213
FLWTR LPLGE---EGDELIERV IEPAFIDYLQIYVNLVAEA--EPVSDRA : 214
FLWTR LPLSK---ESDNIISEI LRPAFGEYLSLYIELLHIA--KPLKKERA : 213
ILWTR LAKHQ---DSNLIENQLYDSFKYINLYLKLTLFES--EEVGHGLQ : 209
FLWTRP-----QETAVVETQVFAAFKDY LKAYLDFVEQA--EAVTDSQN : 202
VWTRF-----SSSKEKHKALPSAFLEYQAWLEMTIQV--REEMEP SH : 237
ASMLKIDAE--EDKLESILRDH VSPAAREVLEVLERCVRKEEEKIVVCEE : 271
VWTRFIDCGRGEGTLEEIVGH LASVVKGI LQIWLDTCASD--ASEMEEG : 155
```

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Fig. 10 cont'd.



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	280	*	300	*
PcyA_ANASP :	OOIEA-GOHNYCTSKOOON		DKTRRVLEKAFGVDDAENVMTT	
PcyA_NOSPU :	TQNEA-GOHNYCTKQQQN		DKTRRVLEKAFGPVVAENVMTT	
PcyA_SYNY3 :	LEHRQ-GOIHYYCQQQQKN		DKTRRVLEKAFGEAAERVNSQ	
PcyA_SYNB1 :	IRRYE-GOLSYCLQQKRND		DKTRRVLEKAFEDASADRYIEE	
PcyA_PROME :	IEERINYCKNYCVQOMKN		EKTSLLVLLKYFDKVVVDEKIEK	
Peba_SYNPY :	PEEWKNLQDKYDIYSAER		DPAHGLFTSHFGCKDQSNRELHE	
Peba_SYNB1 :	PGDVERLQNAVQVYSAER		DPAHGLFTSHFGCKEWSDRRELHE	
Peba_PROMA :	PSKVEQLHINYDIYSAER		DPAHGLFKSYFGGTWADQEVRE	
Peba_PROME :	LEQIKNNQIDYOKYSAEK		DPADKLFKTFEGGTATENFINN	
Peba_NOSPU :	IQRTVKAQKDYQOYSADR		DPASGLFSSYFGHEVAERELHE	
Pebb_SYNPY :	EVLQO-GORKYTDYRAEK		DPARGMLTRFHGSEMTAELIHT	
Pebb_SYNB1 :	ELLPS-GOKRYTAYRAEK		DPARGMLTRFYGSEMTESYIHG	
Pebb_PROMA :	LKIDE-GOKAYINRSTK		DPARAMLCRFYGKEMTEDYIHK	
Pebb_PROME :	QELIN-GANDYLNRRDN		DPARPMLSLEFGKDETESLINK	
Pebb_NOSPU :	LVAIKQAQLRYLRYRAEK		DPARGMFKRFYGAEMTEYIYG	
HY2_ARATH :	VRANCEAONKYLTVRAQK		DPGHGELKRLVGEAKAKELLRD	
RCCR_ARATH :	ERMELERRDKSPRKSIE		DOLDLQTFRMEGGEVSRVVA	
RCCR_HORVU :	EREIMVKRDRTVRSKSI		EVOLTANLPRMEGCPDVSGRITAE	
	q Y 1 4 3G 4			

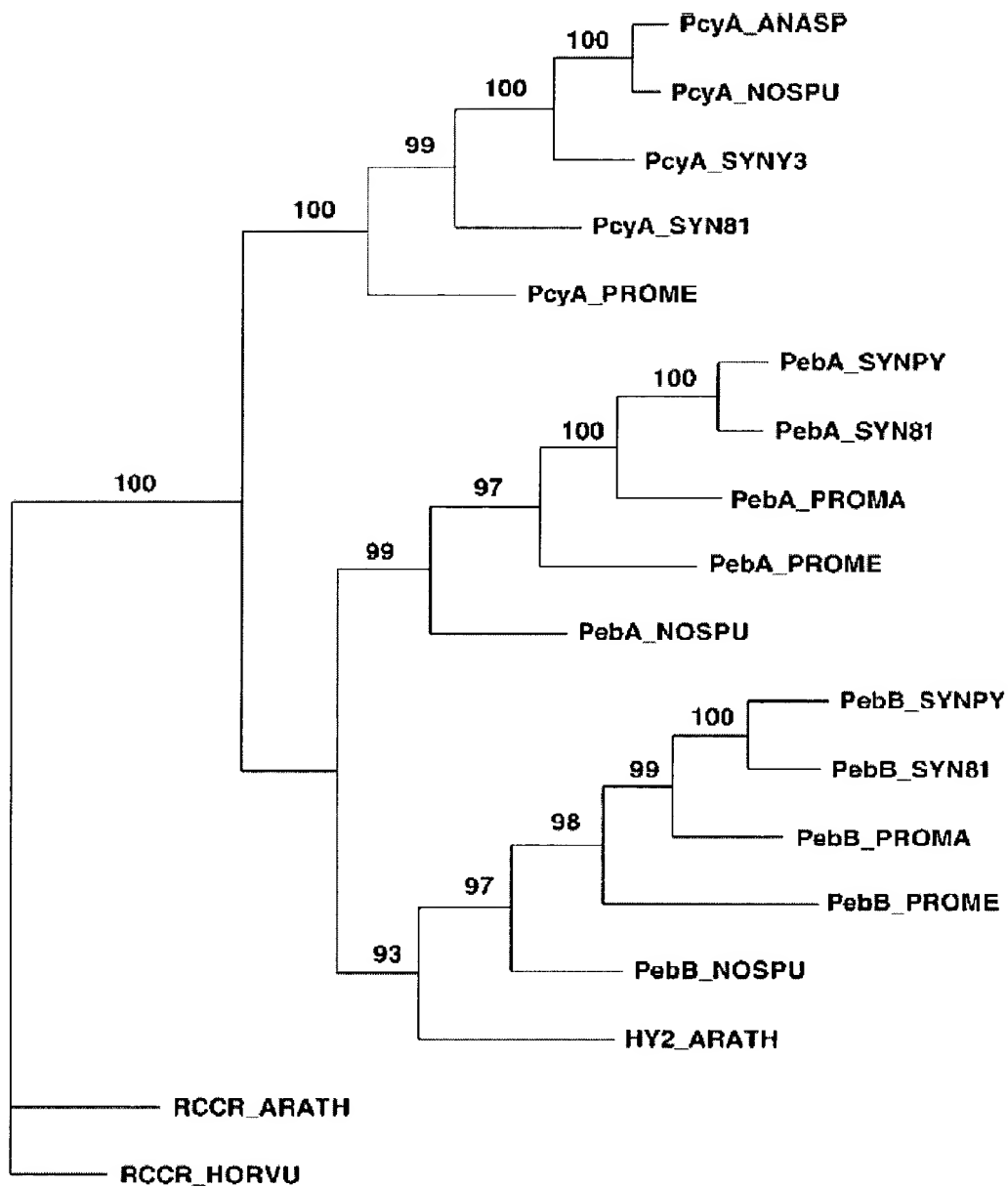
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VLFOLPT----				: 245
VLFQV1Q----				: 248
VLFDPLPFG----				: 247
VLFDF-----				: 243
FLFPASSSHK----				: 236
FLFPASQPA----				: 235
FLFPHSHLTAD----				: 241
FLFTLNHNPLK----				: 236
FLFEDAVPLAVSASKR----				: 280
VLFOL-----				: 257
VLFOLEDAA----				: 262
VLFNI-----				: 257
VLFSTNKVL----				: 257
FLFOLERKLTVVK----				: 255
FLFNGVDELGTRTFIDYFPEYQTE		DTVSDKRSI	IGKSYETR	PWDLTGQFIG : 329
TRKAFGVL-----				: 319
TRKAFGVQEG----				: 205
LF				

Fig. 10 cont'd.



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**Fig. 11**





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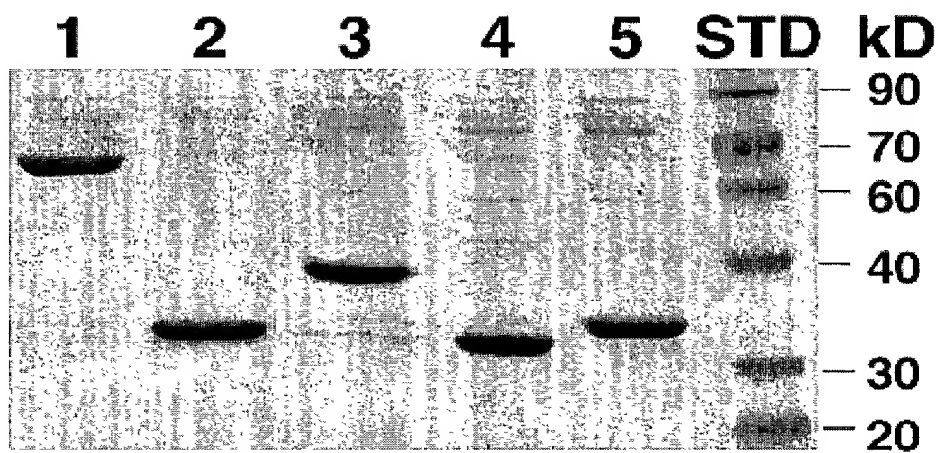
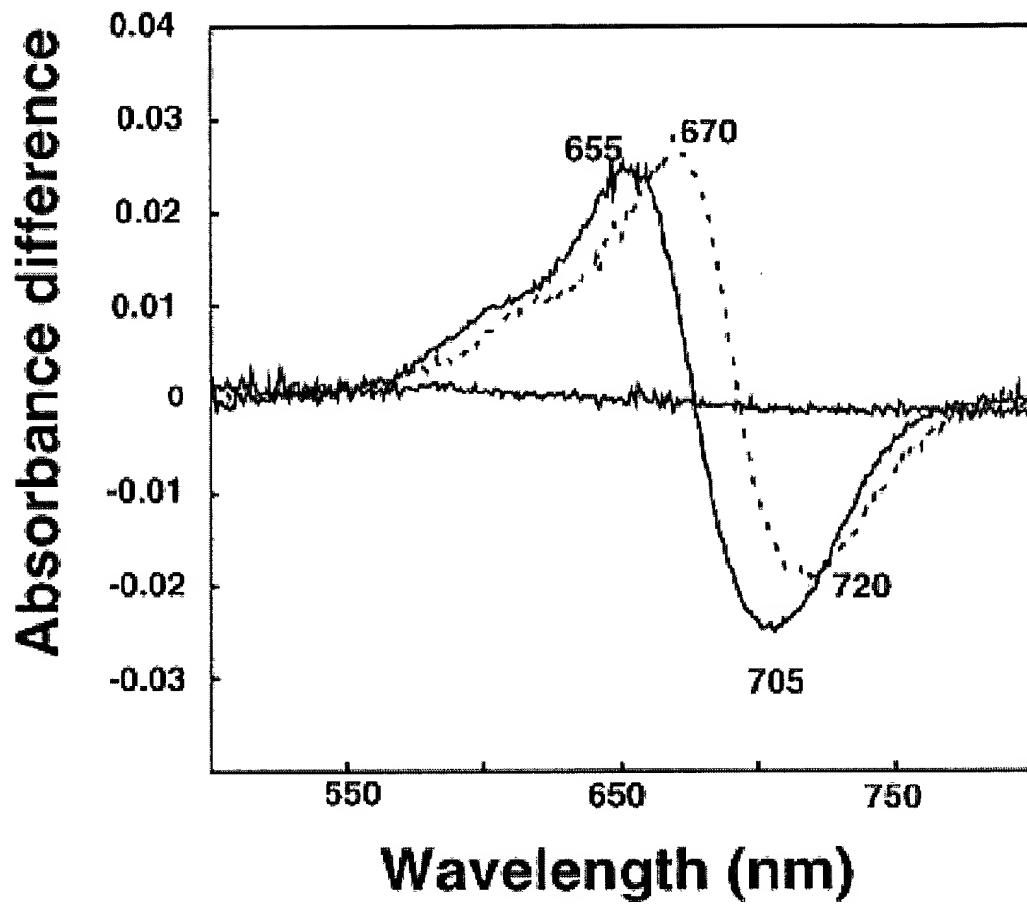


Fig. 12

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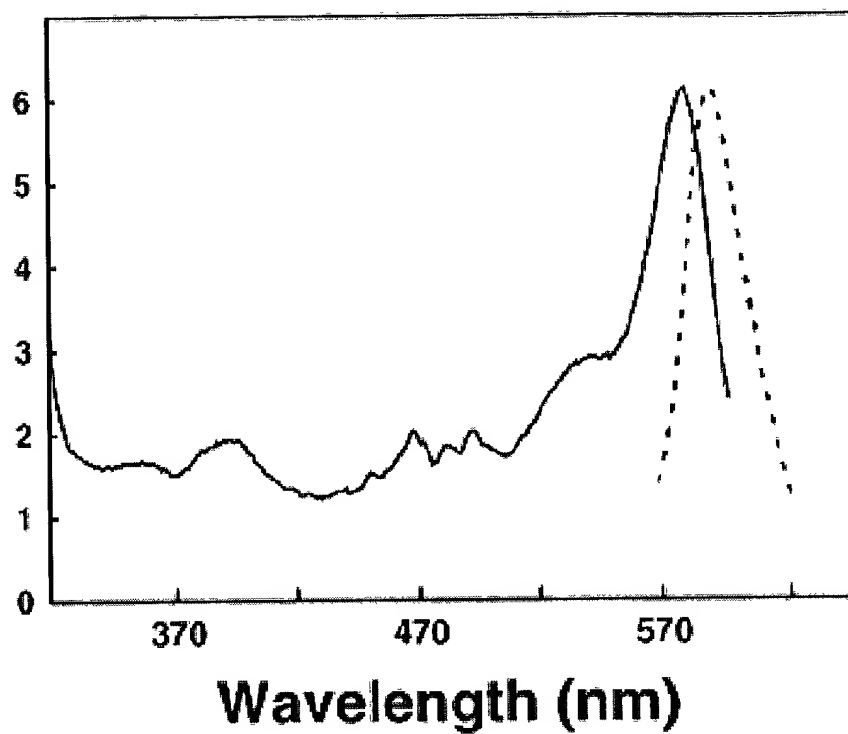
**Fig. 13A**



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Normalized fluorescence

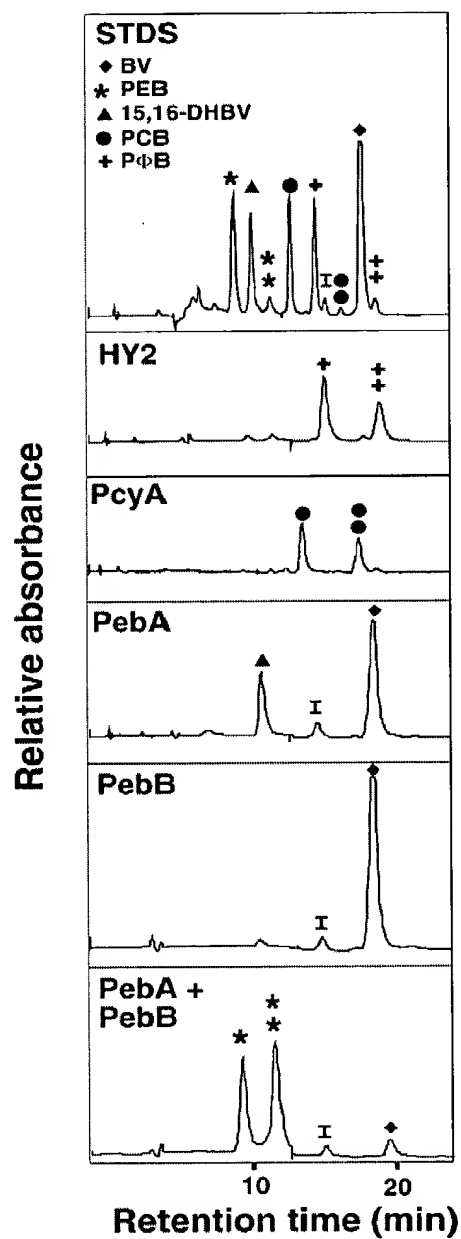


*Fig. 13B*



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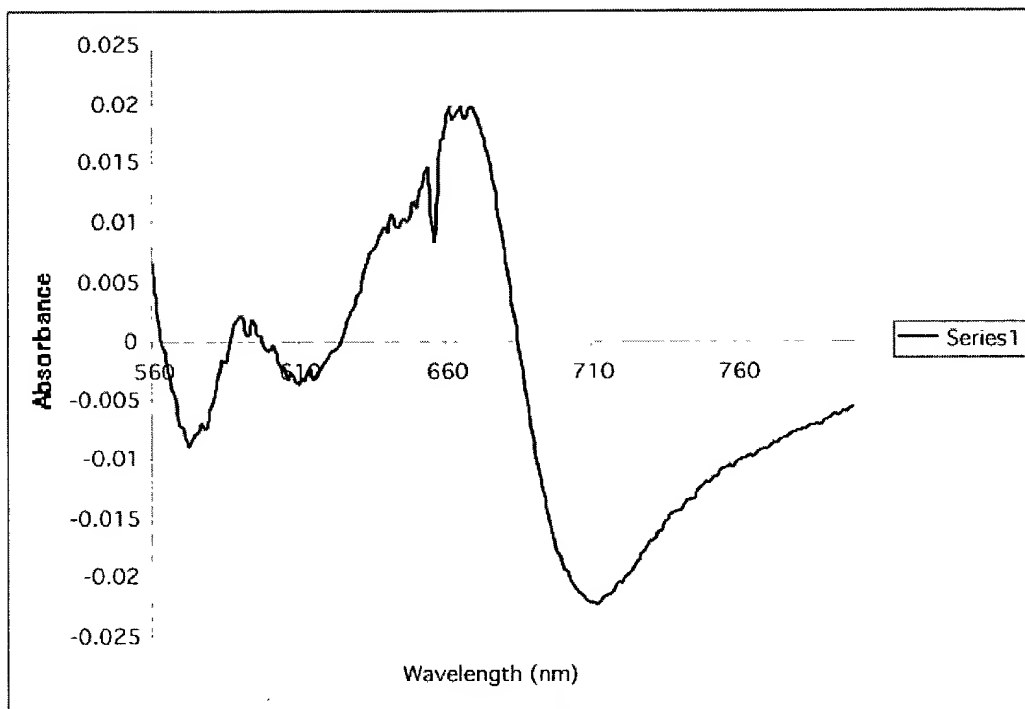


**Fig. 14**



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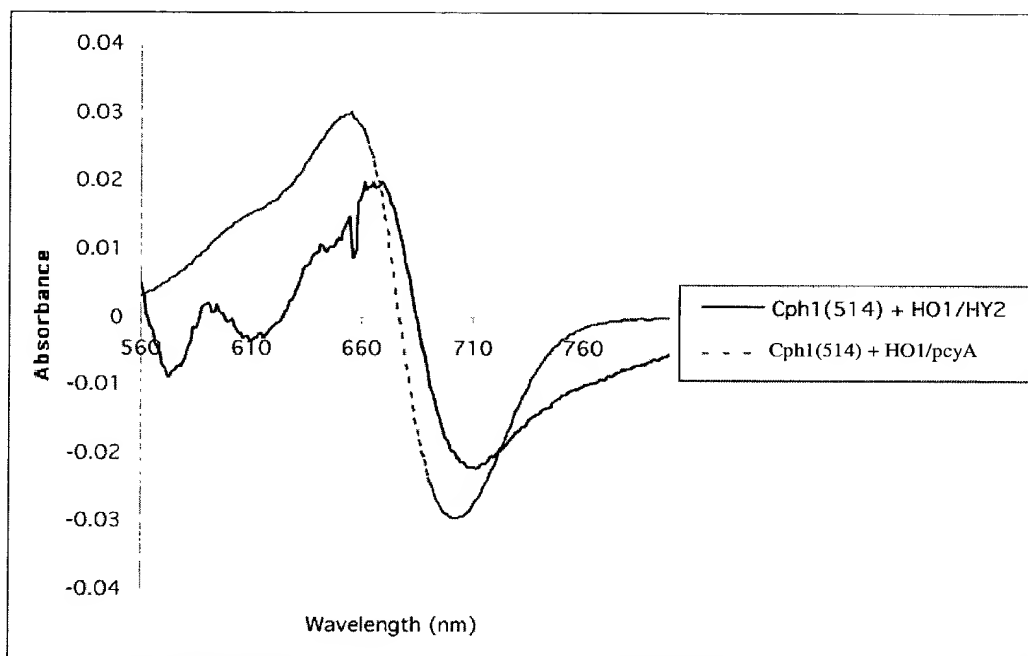


**Fig. 15**



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**Fig. 16**